

## SEQUENCE LISTING

<110> Rhône-Poulenc Rorer

5 <120> Polypeptides capable of interacting with  
oncogenic mutants of the p53 protein

<130> Sequences

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<150> FR9812754

<151> 1998-10-12

15 <160> 33

<170> PatentIn Ver. 2.1

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<213> Artificial sequence

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25 <223> Artificial sequence description: oligonucleotide

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agatctgtat ggaggagccg cag

23

<210> 2

30 <211> 29

<212> DNA

<213> Artificial sequence

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<223> Artificial sequence description: 3'-393  
oligonucleotide (p53)

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29

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<211> 15

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<213> Artificial sequence

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<223> Artificial sequence description: 3' H175  
oligonucleotide

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<210> 4

<211> 15

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<223> Artificial sequence description: 3' W248  
oligonucleotide

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<210> 5

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<213> Artificial sequence

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<223> Artificial sequence description: 3' H273  
oligonucleotide

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<213> Artificial sequence

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<220>  
<223> Artificial sequence description: 3' G281  
oligonucleotide

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<400> 6  
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<210> 7  
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<220>  
<223> Artificial sequence description: 5'-73  
oligonucleotide

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<400> 7  
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<210> 8  
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<221> CDS

<222> (1) .. (885)

<220>

<223> Artificial sequence description: murine MBP1  
5 C-term fragment

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ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg	96
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu	
20 25 30	
ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct	144
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro	
35 40 45	
aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca	192
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro	
50 55 60	
tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt	240
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys	
65 70 75 80	
aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat atc	288
Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile	
85 90 95	
gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc aac	336
Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn	
100 105 110	
gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg ctg	384
Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu	
115 120 125	
gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca cac	432
Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His	
130 135 140	
caa tgt tct gag ggc caa acc tgt gtc aac ttc cat ggg ggt tac cgc	480
Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg	
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tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca gac	528
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp	
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aac cgc tgc ctc tgc cct gcc tcc aat ccc ett tgt cga gag cag cct	576
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro	
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tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt gtg	624
Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val	
195 200 205	
cct gct gac gtg ttc cag atc cag gca acc tct gtc tac cct ggt gcc	672

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
 210 215 220

tac aat gcc ttt cag acc cgt tct gga aac aca cag ggg gac ttc tac 720  
 Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr  
 225 230 235 240

att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg cca 768  
 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
 245 250 255

gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc atg 816  
 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
 260 265 270

aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg gtc 864  
 Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
 275 280 285

ttt gtg gga gcc tat acc ttc tgaagaccct cagggaaaggg ccatgtgggg 915  
 Phe Val Gly Ala Tyr Thr Phe  
 290 295

gcccccttccc cctcccatag ctttaaggcagc cccggggggcc tagggatgac cgttctgctt 975  
 aaaggaacta tgatgtgaag gacaataaag ggagaaaagaa ggaaaaa. 1021

<210> 9

<211> 295

5 <212> PRT

<213> Artificial sequence

<223> Artificial sequence description: murine MBP1  
 C-term fragment

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 Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
 35 40 45  
 Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
 50 55 60  
 Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
 65 70 75 80  
 Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
 85 90 95  
 Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
 100 105 110  
Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
 115 120 125  
 Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His  
 130 135 140  
 Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg  
 145 150 155 160  
 Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp  
 165 170 175  
 Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
 180 185 190  
 Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val  
 195 200 205  
 Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
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 Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr  
 225 230 235 240  
 Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
 245 250 255  
 Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
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 290 295

<210> 10  
<211> 39  
<212> DNA  
<213> Artificial sequence

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<220>  
<223> Artificial sequence description: 5' c-myc  
oligonucleotide

<400> 10  
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39

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<210> 11  
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<212> DNA  
<213> Artificial sequence

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<220>  
<223> Artificial sequence description: 3' c-myc  
oligonucleotide  
<400> 11

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gat c t c a g g t c t c c t c g g a g a t c a g c t t c t g c t c c a t g

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<210> 12  
<211> 45  
<212> DNA  
<213> Artificial sequence

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<223> Artificial sequence description: 5' MCS  
30 oligonucleotide

<400> 12  
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<210> 13  
35 <211> 37

<212> DNA

<213> Artificial sequence

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5 <223> Artificial sequence description: 3' MCS  
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<400> 13

cgcgccgc cccggaaatt gcatgcagg cgaccga

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10 <210> 14

<211> 22

<212> DNA

<213> Artificial sequence

15 <220>

<223> Artificial sequence description: 3' mMBP1  
oligonucleotide

<400> 14

cggtactggc agaggtaact gg

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<210> 15

<211> 1513

<212> DNA

<213> Artificial sequence

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<221> CDS

<222> (49)..(1377)

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<223> Artificial sequence description: murine MBP1  
(complete sequence)

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Met Leu Pro

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Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu		
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ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc	10	153
Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser		
20	25	30
25	30	35
tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac	10	201
Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His		
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45	50	55
tgc cgg gat gtc aac gag tgc ctg acc att ccg gag gct tgc aag ggt	10	249
Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly		
55	60	65
60	65	70
gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc	10	297
Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys Leu Pro Arg		
70	75	80
75	80	85
tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca	10	345
Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro		
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820	825	830
830	835	840
840	845	850
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870	875	880
880	885	890
890	895	900
900	905	910
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930	935	940
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950	955	960
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970	975	980
980	985	990
990	995	1000

230

235

240

atc gac gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc 825  
 Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val  
 245 250 255

aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg 873  
 Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu  
 260 265 270 275

ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca 921  
 Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala  
 280 285 290

cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac 969  
 His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr  
 295 300 305

cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca 1017  
 Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser  
 310 315 320

gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag 1065  
 Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln  
 325 330 335

cct tca tcc att gtg cac cgc tac atg agc acc tca gag cga agt 1113  
 Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser  
 340 345 350 355

gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt 1161  
 Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly  
 360 365 370

gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc 1209  
 Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe  
 375 380 385

tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg 1257  
 Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg  
 390 395 400

cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc 1305  
 Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr  
 405 410 415

atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg 1353  
 Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr  
 420 425 430 435

gtc ttt gtg gga gcc tat acc ttc tgaagaccc tggggaggg ccatgtgggg 1407  
 Val Phe Val Gly Ala Tyr Thr Phe  
 440

gcccccttcccc cctcccatag cttaaaggcagc cccggggggcc tagggatgac cgttctgctt 1467

aaaggaaacta tggatgtgaag gacaataaag ggagaaaagaa ggaaaa 1513

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<211> 443  
<212> PRT  
<213> Artificial sequence  
5 <223> Artificial sequence description: murine MBP1  
(complete sequence)

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Phe Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu  
 20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp  
 35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
 50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
 65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro  
 85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly  
 100 105 110

Tyr Glu Pro Asp Glu Glu Ser Cys Val Asp Val Asp Glu Cys Thr  
 115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
 130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
 145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
 165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
 180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
 195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
 210 215 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
 225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr  
 245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
 260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
 275 280 285

Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
 290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val  
 305 310 315 320

Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
 325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser  
 340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
 355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln  
 370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
 385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
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Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
 420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
 435 440

<210> 17

<211> 21

5 <212> DNA

<213> Artificial sequence

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<223> Artificial sequence description: 3' hMBP1

10 oligonucleotide

<400> 17

ctcccgctccg aggtgatggc

21

<210> 18

15 <211> 21

<212> DNA

<213> Artificial sequence

&lt;220&gt;

<223> Artificial sequence description: 5' hMBP1  
oligonucleotide

5

&lt;400&gt; 18

tgttagctact ccagctacct c

21

&lt;210&gt; 19

&lt;211&gt; 1122

10 &lt;212&gt; DNA

&lt;213&gt; Artificial sequence

&lt;220&gt;

<223> Artificial sequence description: human MBP1 cDNA  
15 (partial sequence)

&lt;400&gt; 19

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cttgggatca gettcttcaggatctga agagcccgac agctacacgg aatgcacaga 180
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&lt;210&gt; 20

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&lt;212&gt; DNA

&lt;213&gt; Artificial sequence

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<223> Artificial sequence description: human MBP1 cDNA  
(partial sequence)

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<210> 21  
<211> 1480  
<212> DNA  
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<220>  
<221> CDS  
<222> (59) .. (1387)

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<220>  
<223> Artificial sequence description: human MBP1  
(complete sequence)

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 Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
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 ctg cta ctg ttg ctc ttg gga tca gct tct cct cag gat tct gaa gag 154  
 Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu  
 20 25 30  
 ccc gac agc tac acg gaa tgc aca gat ggc tat gag tgg gac cca gac 202  
 Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp  
 35 40 45  
 agc cag cac tgc cgg gat gtc aac gag tgt ctg acc atc cct gag gcc 250  
 Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
 50 55 60  
 tgc aag ggg gaa atg aag tgc atc aac cac tac ggg ggc tac ttg tgc 298  
 Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
 65 70 75 80  
 ctg ccc cgc tcc gct gcc gtc atc aac gac cta cac ggc gag gga ccc 346  
 Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro  
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 Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala  
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 Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
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 ggc tcc tat cag tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc 538  
 Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
 145 150 155 160  
 gag tgt gtg gac ata gac gag tgc cgc tac cgc tac tgc cag cac cgc 586  
 Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
 165 170 175  
 tgc gtg aac ctg cct ggc tcc ttc cgc tgc cag tgc gag ccc ggc ttc 634

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe			
180	185	190	
cag ctg ggg cct aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac			682
Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp			
195	200	205	
atg ggg gcc cca tgc gag cag cgc tgc tcc aac tcc tat ggg acc ttc			730
Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe			
210	215	220	
ctg tgt cgc tgc cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc			778
Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser			
225	230	235	240
tgc agt gat att gat gag tgt agc tac tcc agc tac ctc tgt cag tac			826
Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Tyr Leu Cys Gln Tyr			
245	250	255	
cgc tgc gtc aac gag cca ggc cgt ttc tcc tgc cac tgc cca cag ggt			874
Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly			
260	265	270	
tac cag ctg ctg gcc aca cgc ctc tgc caa gac att gat gag tgt gag			922
Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu			
275	280	285	
tct ggt gcg cac cag tgc tcc gag gcc caa acc tgt gtc aac ttc cat			970
Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His			
290	295	300	
ggg ggc tac cgc tgc gtc gac acc aac cgc tgc gtg gag ccc tac atc			1018
Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile			
305	310	315	320
cag gtc tct gag aac cgc tgt ctc tgc ccg gcc tcc aac cct cta tgt			1066
Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys			
325	330	335	
cga gag cag cct tca tcc att gtg cac cgc tac atg acc atc acc tcg			1114
Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser			
340	345	350	
gag cgg agc gtg ccc gct gac gtg ttc cag atc cag gcg acc tcc gtc			1162
Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val			
355	360	365	
tac ccc ggt gcc tac aat gcc ttt cag atc cgt gct gga aac tcg cag			1210
Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln			
370	375	380	
ggg gac ttt tac att agg caa atc aac aac gtc agc gcc atg ctg gtc			1258
Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val			
385	390	395	400
ctc gcc cgg ccg gtg acg ggc ccc cgg gag tac gtg ctg gac ctg gag			1306
Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu			
405	410	415	

atg gcc acc atg aat tcc ctc atg agc tac cgg gcc agc tct gta ctg 1354  
Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
420 425 430

agg ctc acc gtc ttt gta ggg gcc tac acc ttc tgaggagcag gagggagcca 1407  
Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
435 440

ccctccctgc agctacccta gctgaggagc ctgttgtgag gggcagaatg agaaaggcaa 1467  
taaaggaga aag 1480

<210> 22  
5 <211> 443  
<212> PRT  
<213> Artificial sequence  
<223> Artificial sequence description: human MBP1  
(complete sequence)

&lt;400&gt; 22

Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala  
1 5 10 15

Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu  
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp  
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala  
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys  
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro  
85 90 95

Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly  
100 105 110

Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala  
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro  
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro  
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg  
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe  
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp  
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe  
 210 215 220  
 Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser  
 225 230 235 240  
 Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr  
 245 250 255  
 Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly  
 260 265 270  
 Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu  
 275 280 285  
 Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His  
 290 295 300  
 Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile  
 305 310 315 320  
 Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys  
 325 330 335  
 Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser  
 340 345 350  
 Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val  
 355 360 365  
 Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln  
 370 375 380  
 Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val  
 385 390 395 400  
 Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu  
 405 410 415  
 Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu  
 420 425 430  
 Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe  
 435 440

<210> 23  
 5 <211> 817  
 <212> DNA  
 <213> Artificial sequence

<220>

<223> Artificial sequence description: murine MBP1  
cDNA (partial sequence)

<400> 23  
gctgtggcag aaacccctga cttctgccccca ccaccccccac gcctcaggat gctccctttt 60  
gcctcctggcc tccccgggtc tttgtgtgtc tgggggtttc tgctgttgct cttgggagca 120  
gctgtccccac aggtccccga ggagccggac agctacacagg aatgcacaga tggctatgag 180  
tgggatgcag acagccagca ctgccccggat gtcaacgagt gcctgaccat cccggaggct 240  
tgcaagggtg agatgaaatg catcaaccac tacgggggtt atttgtgtct gcctcgctct 300  
gctgtccgtca tcagtgtatcc ccatggtgaa ggacccac cgtccagggc ccatgtctaa 360  
caacccaaacc cttggccgca gggctacgag cctgtatgtac aggagatgtg tggatgtg 420  
gacgagtgtt cccaggctt gcatgactgt cggccctagtc aggactgcca taacccctt 480  
ggctccctacc agtgcacccgt ccctgtatgtt tacggaaaaa ttggaccccgaa atgtgtggac 540  
atagatgagt gtcgttacccg ctattggccag catcgatgtg tgaacccgtcc gggctctttt 600  
cgatgccagt gtgagccagg cttccagttt ggacctaaca accgttcttg tggatgtg 660  
aatgagtgtg acatggggc cccatgtgag cagcgctgtc tcaacttcta tgggacccctt 720  
ctgtgtcgct gtaaccagggtt atatgagctg caccggatgtg gcttctctgt cagcgatatac 780  
gatgagtgtcg gtcactccat ttacccctgtc cagtacc 817

5

<210> 24  
<211> 24  
<212> DNA  
<213> Artificial sequence

10

<220>  
<223> Artificial sequence description: sense-GAPDH  
oligonucleotide

15

<400> 24  
cgaggatcaac ggatttggcc gtat 24

20 <213> Artificial sequence

<220>  
<223> Artificial sequence description: antisense-GAPDH  
oligonucleotide

25

<400> 25  
agcccttctcc atgggtgggtga agac

24

<210> 26  
<211> 25  
<212> DNA  
<213> Artificial sequence

5

<220>  
<223> Artificial sequence description: oligonucleotide

<400> 26  
cggttggcct tggggttcag ggggg

25

10

<210> 27  
<211> 21  
<212> DNA  
<213> Artificial sequence

15

<220>  
<223> Artificial sequence description: sense MBP1  
oligonucleotide

20

<400> 27  
gcctcgatgg ttacccgaag a

21

<210> 28  
<211> 21  
<212> DNA  
<213> Artificial sequence

30

<220>  
<223> Artificial sequence description: antisense MBP1  
oligonucleotide

<400> 28  
agccccccatg gaaggttgaca c

21

<210> 29  
<211> 20

<212> DNA

<213> Artificial sequence

<220>

5 <223> Artificial sequence description: sense-actin  
oligonucleotide

<400> 29

gtggggcgcc ccagggacca

20

10 <210> 30

<211> 1358

<212> DNA

<213> Artificial sequence

15 <220>

<221> CDS

<222> (1) .. (885)

<220>

20 <223> Artificial sequence description: human MBP1  
C-term fragment

<400> 30

tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc gag tgt gtg gac 48  
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15

ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtg aac ctg 96  
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30

cct ggc tcc ttc cgc tgc cag tgc gag cgc ggc ttc cag ctg ggg cct 144  
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45

aac aac cgc tcc tgt gtt gat gtc aac gag tgt gac atg	ggg gcc cca	192	
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met	Gly Ala Pro		
50	55	60	
tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc	ctg tgt cgc tgc	240	
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe	Leu Cys Arg Cys		
65	70	75	80
cac cag ggc tat gag ctc cat cgg gat ggc ttc tcc	tgc agt gat att	288	
His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys	Ser Asp Ile		
85	90	95	
gat gag tgt agc tac tcc agc tac ctc tgt cag tac	cgc tgc gtc aac	336	
Asp Glu Cys Ser Tyr Ser Tyr Leu Cys Gln Tyr Arg	Cys Val Asn		
100	105	110	
gag cca ggc cgt ttc tcc tgc cac tgc cca cag ggt	tac cag ctg ctg	384	
Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly	Tyr Gln Leu		
115	120	125	
gcc aca cgc ctc tgc caa gac att gat gag tgt gag	tct ggt gcg cac	432	
Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser	Gly Ala His		
130	135	140	
cag tgc tcc gag gcc caa acc tgt gtc aac ttc cat	ggg ggc tac cgc	480	
Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His	Gly Gly Tyr Arg		
145	150	155	160
tgc gtg gac acc aac cgc tgc gtg gag ccc tac atc	cag gtc tct gag	528	
Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile	Gln Val Ser Glu		
165	170	175	
aac cgc tgt ctc tgc ccg gcc tcc aac cct cta	tgt cga gag cag cct	576	
Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys	Arg Glu Gln Pro		
180	185	190	
tca tcc att gtg cac cgc tac atg acc acc tcg	gag cgg agc gtg	624	
Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser	Glu Arg Ser Val		
195	200	205	
ccc gct gac gtg ttc cag atc cag gcg acc tcc	gtc tac ccc ggt gcc	672	
Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val	Tyr Pro Gly Ala		
210	215	220	
tac aat gcc ttt cag atc cgt gct gga aac tcg	cag ggg gac ttt tac	720	
Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln	Gly Asp Phe Tyr		
225	230	235	240
att agg caa atc aac aac gtc agc gcc atg	ctg gtc ctc gcc cgg ccc	768	
Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val	Leu Ala Arg Pro		
245	250	255	
gtg acg ggc ccc cgg gag tac gtg ctg gac	ctg gag atg gtc acc atg	816	
Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu	Met Val Thr Met		
260	265	270	
aat tcc ctc atg agc tac cgg gcc agc tct gta	ctg agg ctc acc gtc	864	
Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val	Leu Arg Leu Thr Val		

275

280

285

ttt gta ggg gcc tac acc ttc tgaggagcag gagggagcca ccctccctgc 915  
 Phe Val Gly Ala Tyr Thr Phe  
 290 295

agctacccta gctgaggagc ctgttgtgag gggcagaatg agaaaggcaa taaaggaga 975  
 aagaaaagtcc tggggctga ggtggggcggg tcacactgca ggaaggctca ggctggggca 1035  
 gggggggact tggggggggca ggccaaagtcc acctaaatgg gggctcttat atgttcaggc 1095  
 ccagggggccc ccattgacag gagctgggag ctctgcacca cgagcttcag tcaccccgag 1155  
 aggagaggag gtaacgagga gggcggactc cagggcccccgg cccagagatt tggacttggc 1215  
 tggcttcag gggctctaag aaactccact ctggacagcg ccaggaggcc ctgggttcca 1275  
 ttcctaactc tgcctcaaac tgcacatttgcataagccct agtagttccc tgggcctgtt 1335  
 ttctataaaa acgaggcaac tgg 1358

&lt;210&gt; 31

&lt;211&gt; 295

5 &lt;212&gt; PRT

&lt;213&gt; Artificial sequence

<223> Artificial sequence description: human MBP1  
 C-term fragment

&lt;400&gt; 31

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp  
1 5 10 15Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu  
20 25 30Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro  
35 40 45Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro  
50 55 60Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys  
65 70 75 80His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile  
85 90 95Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn  
100 105 110Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu  
115 120 125Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His  
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg

145

150

155

160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu  
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro  
180 185 190

Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val  
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala  
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr  
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro  
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met  
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val  
275 280 285

Phe Val Gly Ala Tyr Thr Phe  
290 295

<210> 32

<211> 1663

<212> DNA

5 <213> Artificial sequence

<220>

<221> CDS

<222> (1)..(999)

10

<220>

<223> Artificial sequence description: murine fibulin  
2 c-term fragment

&lt;400&gt; 32

gag ggc tct gaa tgt gtg gat gtg aat gag tgt gag aca ggt gtg cat 48  
Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His  
1 5 10 15

cgc tgt ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc 96  
Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg  
20 25 30

tgt gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc 144  
Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys  
35 40 45

att gat gtg aac gaa tgc tgg gtc tcg cag ggc cgc ctg tgc cag cac 192  
Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His

50

55

60

aca tgt gag aac aca ccc ggc tcc tac cgc tgc tcc tgc gct gct ggc	240
Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly	
65 70 75 80	
tcc ctt ttg gcc gca gat ggc aaa cat tgt gaa gat gtg aac gag tgc	288
Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys	
85 90 95	
gag act cgg cgc tgc agc cag gaa tgt gcc aac atc tat ggc tcc tat	336
Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr	
100 105 110	
cag tgc tac tgc cgt cag ggc tac cag ctg gca gag gat ggg cat acc	384
Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr	
115 120 125	
tgc aca gac atc gat gag tgt gca cag ggc gcg ggc att ctc tgt acc	432
Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Ile Leu Cys Thr	
130 135 140	
ttc cgc tgt gtc aac gtg cct ggg agc tac cag tgt gca tgc cca gag	480
Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu	
145 150 155 160	
caa ggg tat aca atg atg gcc aac ggg agg tcc tgc aag gac ctg gat	528
Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp	
165 170 175	
gag tgt gca ctg ggc acc cac aac tgc tct gag gct gag acc tgc cac	576
Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His	
180 185 190	
aat atc cag ggg agt ttc cgc tgc ctg cgc ttt gat tgt cca ccc aac	624
Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn	
195 200 205	
tat gtc cgt gtc tca caa acg aag tgc gag cgc acc aca tgc cag gat	672
Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp	
210 215 220	
atc acg gaa tgt caa acc tca cca gct cgc atc acg cac tac cag ctc	720
Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu	
225 230 235 240	
aat ttc cag aca ggc cta ctg gta cct gca cat atc ttc cgc atc ggc	768
Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly	
245 250 255	
cct gct ccc gcc ttt gct ggg gac acc atc tcc ctg acc atc acg aag	816
Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys	
260 265 270	
ggc aat gag gag ggc tac ttc gtc aca cgc aga ctc aat gcc tac act	864
Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr	
275 280 285	
ggg gtc gta tcc ctg cag cgg tct gtc ctg gag ccc cgg gac ttt gcc	912

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala  
 290 295 300

cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc 960  
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
 305 310 315 320

ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgagggtgaca 1009  
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro  
 325 330

tgtcaggcaa tccctccagg tcatgcctgg gcgggtggca gctgcgcac tcctaagtgg 1069  
 ctttttgcgt tgactctgtta acttaactta atcatgtga gctgggtgggt ctggagcttc 1129  
 tacccctagag ggagggagat gcaccccagc aggcactgag tacaggccag ggtcacccga 1189  
 ggcttagatgg tgacccgtcaa actggaaaca gccatagggg gcttctgaac tccactcttc 1249  
 aactatggct acagctgaca tcccatcttc tcatccactg ttttcttcaa taaaaaaaaa 1309  
 aaatcagctg tgcatggtag cacagaccc taaatccctgc actggggagg cagaggttagg 1369  
 tagatctctg agttccaggg cagcctggtc tacactggga gttctaacca gccagagcta 1429  
 catagagaga ccctatctca acaaggaaaa aacgaaagaa atctctgtga gttccaggcc 1489  
 agcctggct acgctggag ttcttaaccag ccagagctac atagagagat cctatctcaa 1549  
 caaggaaaaa taaaagaaaat cattttaaa ggtttttttt tttgtgttg ttttttaatg 1609  
 ataagagtag cacatataca ttataaaaa tgatcaaata gcacagaaaag gttt 1663

<210> 33

<211> 333

5 <212> PRT

<213> Artificial sequence

<223> Artificial sequence description: murine fibulin  
 2 c-term fragment

&lt;400&gt; 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His  
1 5 10 15Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg  
20 25 30Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys  
35 40 45Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His  
50 55 60Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly  
65 70 75 80Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys  
85 90 95

Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr  
 100 105 110  
 Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr  
 115 120 125  
 Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr  
 130 135 140  
 Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu  
 145 150 155 160  
 Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp  
 165 170 175  
 Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His  
 180 185 190  
 Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn  
 195 200 205  
 Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp  
 210 215 220  
 Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu  
 225 230 235 240  
 Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly  
 245 250 255  
 Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys  
 260 265 270  
 Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr  
 275 280 285  
 Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala  
 290 295 300  
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe  
 305 310 315 320  
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro  
 325 330